

TITLE
JOURNAL
MEDLINE
COMMENT

Brustein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J., and Simpson, A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 20202663
 Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo, SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707901
 Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?C1-RC5St2-RC5-GN0281>)
 Seq primer: puc 18 forward
 High quality sequence step: 214.

FEATURES
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="GN0281"
 /dev_stage="Adult"
 /note="Organ: placenta.normal; Vector: puc18; Site_1: SmaI ; Site_2: SmaI; A mini-library was made by cloning products derived from ORFEST PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
 BASE COUNT 67 a 36 c 88 g 23 t
 ORIGIN

Alignment Scores:
 Pred. No.: 0.0168 Length: 214
 Score: 60.00 Matches: 12
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 Gaps: 0

US-09-856-070-21 (1-12) x B1054475 (1-214)
 Q7 1 GlutathioneS-transferase gamma 12
 |||||
 Db 56 CAGGAGTGAATGCTGGCGCTGCAGAGCTATGAGGAG 91

RESULT 2
 B1054475
 LOCUS B1054475 214 bp mpna linear EST 15 JUN 2001
 DEFINITION RC5-GN0281: clone 012 H01 GN0281 Homo sapiens cDNA, mRNA sequence.
 ACCESSION B1054475
 VERSION B1054475.1 GI:14462005
 EST.
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE
 AUTHORS
 1 (bases 1 to 214)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Naei, M.A., da Silva, W. Jr., Zacc, M.A., Bordin, S., Costa, F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brustein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J., and Simpson, A.J.
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COMMENT

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 (<http://www.ludwig.org.br/scripts/gethtml2.pl?C1-RC5-GN0281>)
 Seq primer: puc 18 forward
 High quality sequence step: 214.

FEATURES

source
 1..214
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="GN0281"
 /dev_stage="Adult"
 /note="Organ: placenta.normal; Vector: puc18; Site_1: SmaI ; Site_2: SmaI; A mini-library was made by cloning products derived from ORFEST PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
 BASE COUNT 68 a 36 c 88 g 22 t
 ORIGIN

Alignment Scores:
 Pred. No.: 0.0168 Length: 214
 Score: 60.00 Matches: 12
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 Gaps: 0

US-09-856-070-21 (1-12) x B1054475 (1-214)
 Q7 1 GlutathioneS-transferase gamma 12
 |||||
 Db 56 CAGGAGTGAATGCTGGCGCTGCAGAGCTATGAGGAG 91

RESULT 3
 B0367833/c
 LOCUS B0367833 215 bp mRNA linear EST 21-MAY-2002
 DEFINITION RC5-GN0281: clone 013 AC9 GN0281 Homo sapiens cDNA, mRNA sequence.
 ACCESSION B0367833
 VERSION B0367833.1 GI:21043334
 EST.
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE
 AUTHORS
 1 (bases 1 to 215)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Naei, M.A., da Silva, W. Jr., Zacc, M.A., Bordin, S., Costa, F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brustein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J., and Simpson, A.J.
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 Tel: +55-11-2704922
 Fax: +55-11-2707901

Site_2: ECOR1;

Toplog' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

BASE COUNT 81 a 48 c 117 g 29 t
ORIGIN

Alignment Scores:

Pred. No.: 0.0241 Length: 276
Score: 60.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-09-856-070-21 (1-12) x BMR44124 (1-276)

OY 1 C10C10151-031100-513-105 C10151 Homo sapiens cDNA, mRNA sequence.
Db 48 GAGAGGTGATGCTGGGGTGGAGAGTATGAGGAG 83
|||||

RESULT 1 6

BF804323

LOCUS BF804323 276 bp mRNA linear EST 12 JAN 2001

DEFINITION QV4-C10151-031100-513-105 C10151 Homo sapiens cDNA, mRNA sequence.

ACCESSION BF804323

VERSION BF804323.1 GI:12133312

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

1 (bases 1 to 279)

Authors Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, C.H., Carvalho, A.F., Matsukuma, A., Bata, G.S., Simpson, D.H.,

Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare

M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and

Simpson, A.J.

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Brazil

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Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

project. This entry can be seen in the following URL.

(http://www.ludwig.org.br/scripts/getbml2.pl?l=QV4,2-QV4-Q151)

031100-513-105&t3-2000-11-03&t4-1)

Seq primer: puc 18 forward

High quality sequence stop: 279.

Location/Qualifiers

1..279

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="C10151"

/dev_stage="Adult"

/note="Organ: colon; ins: Vector: puc18; Site_1: Small;

Site_2: Small; A mini-library was made by cloning products

derived from ORFEST PCR (O.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the puc 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under

low stringency conditions."

BASE COUNT 88 a 53 c 111 g 27 t

ORIGIN

Alignment Scores:

Pred. No.: 0.0249 Length: 281

Score: 60.00 Matches: 12

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 10 Gaps: 0

Pred. No.: 0.0246 Length: 279
Score: 60.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-856-070-21 (1-12) x BF804323 (1-279)

OY 1 C10C10151-031100-513-105 C10151 Homo sapiens cDNA, mRNA sequence.
Db 121 GAGAGGTGATGCTGGGGTGGAGAGTATGAGGAG 156
|||||

RESULT 7

AW845219

LOCUS AW845219 281 bp mRNA linear EST 19 MAY 2000

DEFINITION QV4-C10151-031100-513-105 C10151 Homo sapiens cDNA, mRNA sequence.

ACCESSION AW845219

VERSION AW845219.1 GI:7940736

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

1 (bases 1 to 281)

Authors Dias Neto, E., Garcia Correia, R., Verjovski-Almeida, S., Briones, M.R.,

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, C.H., Carvalho, A.F., Matsukuma, A., Bata, G.S., Simpson, D.H.,

Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare

M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and

Simpson, A.J.

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This sequence was derived from the FAPESP/LICR Human Cancer Genome

project. This entry can be seen in the following URL.

(http://www.ludwig.org.br/scripts/getbml2.pl?l=QV4,2-QV4-Q151)

031100-513-105&t3-1999-06-29&t4-1)

Seq primer: puc 18 forward

High quality sequence start: 10

High quality sequence stop: 280.

Location/Qualifiers

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/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="C10151"

/dev_stage="Adult"

/note="Organ: colon; ins: Vector: puc18; Site_1: Small; Site_2:

Small; A mini-library was made by cloning products derived

from ORFEST PCR (O.S. Letters Patent application No. 196

,716 - Ludwig Institute for Cancer Research)

profiles into the puc 18 vector. Reverse transcription of tissue

mRNA and cDNA amplification were performed under low

stringency conditions."

BASE COUNT 94 a 52 c 105 g 30 t

ORIGIN

Alignment Scores:

Pred. No.: 0.0249 Length: 281

Score: 60.00 Matches: 12

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 10 Gaps: 0

US-09-856-070-21 (1-12) x AW845219 (1 281)

QY 1 Glut1LeuMetLeuArgLeuGlnAspTyrGln 12
 DB 176 CAGGACTTGAACCGCGCTCCAGACATACAGCAG 211

RESULT 8

BI050028/c
 LOCUS BI050028/c 294 bp mRNA linear EST 15-JUN-2001
 DEFINITION CMC GN0294 (c001): 676-bp cDNA, mRNA sequence.
 ACCESSION BI050028
 VERSION BI050028.1 GI:14455558
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nadai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
 Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
 M.J., Soares, F., Brentani, R., Reis, J.F., de Souza, S.J. and
 Simpson, A.J.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc Natl Acad Sci U S A 97 (7), 3491-3496 (2000)
 200202663
 Contact: Simpson A.J.J.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel.: +55-11-2707001
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?1-MC6-2-CM-GN0294-
 020101-676-e08d3-2001-01-03&t4-1)
 Seq primer: puc 18 forward
 High quality sequence start: 17
 High quality sequence stop: 294.

FEATURES
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="GN0294"
 /dev_stage="Adult"
 /note="Organ: placenta_normal; Vector: puc18; Site_1: SmaI
 ; Site_2: SmaI; A mini-library was made by cloning
 products derived from ORESTES PCR (U.S. Letters Patent
 application No. 196,716 - Ludwig Institute for Cancer
 Research) profiles into the puc 18 vector. Reverse
 transcription of tissue mRNA and cDNA amplification were
 performed under low stringency conditions."
 34 a 114 c 56 q 90 t

BASE COUNT
 ORIGIN
 Alignment Scores:
 Pred. No.: 0.0266 Length: 294
 Score: 60.00 Matches: 12
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DH: 13 Gaps: 0

US-09-856-070-21 (1-12) x BI050028 (1 294)
 QY 1 Glut1LeuMetLeuArgLeuGlnAspTyrGln 12
 DB 213 CAGGACTTGAACCGCGCTCCAGACATACAGCAG 178

RESULT 9

BF869430
 LOCUS BF869430 297 bp mRNA linear EST 17-JAN-2001
 DEFINITION QY0-ET0148-231000-456-d07 ET0148 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BF869430
 VERSION BF869430.1 GI:12259560
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Ekjof, M., Metcalen, C., Chardata, Craniata, Vertebrata, Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 297)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nadai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
 Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
 M.J., Soares, F., Brentani, R., Reis, J.F., de Souza, S.J. and
 Simpson, A.J.J.
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 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel.: +55-11-2707001
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?1-MC6-2-CM-ET0148-
 231000-456-d07&t4-2001-01-03&t4-1)
 Seq primer: puc 18 forward
 High quality sequence stop: 297.

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 /db_xref="taxon:9606"
 /clone_lib="ET0148"
 /dev_stage="Adult"
 /note="Organ: lung_tumor; Vector: puc18; Site_1: SmaI;
 Site_2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the puc 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."
 90 a 56 c 119 q 31 t 1 others

BASE COUNT
 ORIGIN
 Alignment Scores:
 Pred. No.: 0.027 Length: 297
 Score: 60.00 Matches: 12
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DH: 12 Gaps: 0

US-09-856-070-21 (1-12) x BF869430 (1-297)
 QY 1 Glut1LeuMetLeuArgLeuGlnAspTyrGln 12
 DB 121 CAGGACTTGAACCGCGCTCCAGACATACAGCAG 156

RESULT 10
 BF827086
 LOCUS BF827086 312 bp mRNA linear EST 06-MAR-2002
 DEFINITION F-ET0148-231000-456-d07 ET0148 Homo sapiens cDNA clone # 5530671 44-609 5',
 mRNA sequence.
 ACCESSION BF827086

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VERSION      BMR27086.1  GI:19183495
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens
REFERENCE    Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
              1 (bases 1 to 312)
              Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
              Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
              Kim, Y.S.
TITLE        21c Frontier Korean EST Project 2001
JOURNAL      Unpublished (2002)
COMMENT      Contact: Kim YS
              Genome Research Center
              Korea Research Institute of Bioscience & Biotechnology
              52 Eoeun-dong, Yusong-gu, Taejeon 305-380, South Korea
              Tel: +82-42-860-4470
              Fax: +82-42-860-4409
              Email: yongsund@mail.krrib.ri.kr
              Plate: 44 row: G column: 09
              High quality sequence stop: 312.
              Location/Qualifiers
FEATURES     source
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              /db_xref="taxon:9606"
              /clone_lib="S9SN0601-44-009"
              /clone_lib="S9SN0601"
              /sex="M"
              /issue_type="Ascites"
              /cell_type="Epithelial"
              /cell_line="SNU-601"
              /lab_host="Top10F"
              /note="Organ: Stomach; Vector: pME18-FL3; Site: 1: XhoI;
              Site: 2: XhoI; The poly (A)+ RNA was dephosphorylated with
              bacterial alkaline phosphatase (BAP) and then dephapped
              with tobacco acid pyrophosphatase (TAP). The dephapped
              infant mRNA was ligated with DNA-RNA linker including SfiI
              site by treatment of 14 PNA ligase and the first strand
              cDNA was synthesized with Superscript II using SfiI
              oligo-dT primer. After first strand synthesis, RNA was
              degraded by NaOH treatment and cDNA was amplified by PCR
              reaction. The PCR products were digested with SfiI and
              cloned into DraIII- digested pME18-FL3 vector. The
              obtained cDNA vectors were used for transformation of
              competent cells E. coli Top10F by electroporation method.
              The cDNA libraries constructed by this method are
              full-length enriched cDNA library"
BASE COUNT   108 a 60 c 110 g 34 t
ORIGIN
Alignment Scores:
Pred. No.: 0.0289 Length: 312
Score: 60.00 Matches: 12
Percent Similarity: 100.00% Conservations: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 14

US 09-856-070-21 (1-12) x BMR27086 (1-312)
CY 1 GAGCAGTTGATGTCGAGCTGAGACTATGAGAGC 250
|||||
10 215 GAGCAGTTGATGTCGAGCTGAGACTATGAGAGC 250
|||||
RESULT 11
BQ323847
LOCUS      CM0-C10095 301000-648-bp5 c10095 Homo sapiens cDNA, mRNA sequence.
DEFINITION BQ323847
ACCESSION  BQ323847
VERSION    BQ323847.1  GI:20935634
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 364)
Dias Nereio, E., Garcia Correa, P., Verjovsky-Almeida, S., Briones, M.R.,
Naqai, M.A., da Silva, W. Jr., Zaqa, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Haba, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jondaneel, C.V., O'Hare
M.J., Soares, F., Bruntani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
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Brazil
Tel: +55-11-2704722
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICP Human Cancer Genome
Project. This entry can be seen in the following URL:
http://www.ludwig.org.br/scripts/getform2.pl?cl=cm0,2-cm0-C10095-
301000-648-bp5&tr=2000-10-30&t4=1
Seq primer: puc 18 forward
High quality sequence stop: 2.
Location/Qualifiers
1..358
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="C10095"
/dev_stage="Adult"
/label="cDNA; Column: Ins; Vector: puc18; Site: 1: SmaI;
Site: 2: SmaI; A mini-library was made by cloning products
derived from OMNIES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT   112 a 74 c 130 g 42 t
ORIGIN
Alignment Scores:
Pred. No.: 0.0353 Length: 358
Score: 60.00 Matches: 12
Percent Similarity: 100.00% Conservations: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 14

US 09-856-070-21 (1-12) x BQ323847 (1-358)
CY 1 GAGCAGTTGATGTCGAGCTGAGACTATGAGAGC 263
|||||
10 228 GAGCAGTTGATGTCGAGCTGAGACTATGAGAGC 263
|||||
RESULT 12
BQ368118
LOCUS      PM3-CN0516-090501-010-d10 GN0516 Homo sapiens cDNA, mRNA sequence.
DEFINITION BQ368118
ACCESSION  BQ368118
VERSION    BQ368118.1  GI:21043632
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 364)
Dias Nereio, E., Garcia Correa, P., Verjovsky-Almeida, S., Briones, M.R.,
Naqai, M.A., da Silva, W. Jr., Zaqa, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Haba, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jondaneel, C.V., O'Hare

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/db_xref="taxon:9606"
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/clone_lib="S4SN01"
/sex="M"
/tissue_type="Stomach"
/cell_type="lymphoblast-like"
/lab_host="Top10F"
/notes="Organ: Stomach; Vector: pTZ18Rpl; Site_1: EcoRI; Site_2: NotI; The poly (A) RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then dephosphated with tobacco acid pyrophosphatase (TAP). The dephosphated intact mRNA was ligated with DNA-RNA linker including EcoRI I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."
BASE COUNT      127 a   83 c   141 q   53 t
ORIGIN
Alignment Scores:
Pred. No.:      0.042      Length:      404
Score:          60.00      Matches:      12
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:             14      Gaps:        0

US-09-856-070-21 (1-12) x HQ300862 (1-413)
QY 1 GluGluLeuMetLeuArgLeuGlnAspTyrGluGlu 12
|||||
DB 273 GAGCACTGATGCTGGCGCTGCAGGACTATGAGGAG 308

RESULT 15
HQ300862/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
COMMENT

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This sequence was derived from the FAPES/UNIC Human Cancer Genome project, this entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?11-MR4&12-MR4-KT0047-160501-003-104&t3-2001-05-16&t4-1)
 Seq primer: puc 18 forward
 High quality sequence stop: 413.

FEATURES
 Location/Qualifiers
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 /clone_lib="KT0047"
 /dev_stage="Adult"
 /note="Organ: bladder tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) puc183 into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 46 a 156 c 86 g 125 t
 ORIGIN

Alignment Scores:
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 Score: 60.00 Matches: 12
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 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 14 Gaps: 0

US-09-856-070-21 (1-12) x HQ300862 (1-413)
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 DB 189 GAGCACTGATGCTGGCGCTGCAGGACTATGAGGAG 154

Search completed: January 16, 2003, 21:37:07
 Job time: 1588.77 secs